AMENDMENTS TO THE CLAIMS

1. (Canceled)

2. (Currently amended) A method according to claim 4, further including determining by means of at least one processor, based on the alignment having the smallest error, a mismatch number based on mismatches between the first sequence and the second sequence.

3. (Original) A method according to claim 2, where: the mismatches are negative matches, and, the matches can be at least one of perfect matches and positive matches.

4. (Currently amended) A method for comparing a first sequence and a second sequence, performed on a suitably programmed computer system containing at least one input device, at least one output device, at least one storage means, and at least one processor, the method comprising:

(a) determining by means of at least one processor a plurality of alignments of the first sequence and the second sequence and, for each said alignment of the first sequence and the second sequence, associating an error with the said alignment of the first sequence and the second sequence,

(b) comparing by means of at least one processor the alignment errors to identify an alignment having a smallest error,

(c) based on the alignment having the smallest error, computing by means of at least one processor: a first percent identity relative to the first sequence, and a second percent identity relative to the second sequence, and

(d) based upon the computed first percent identity and second percent identity, outputting a result by means of at least one output device to at least one of a user, a storage device, a computer, or a display,

where computing a first percent identity relative to the first sequence includes: determining an alignment number based on matches between the first sequence and the second sequence based on the alignment having the smallest error, and forming a ratio based on the alignment number and a length of the first sequence, and,

where outputting a result comprises outputting at least one of a ~~the first~~ percent identity, ~~the second percent identity, a third percent identity,~~ a scoring matrix, an identification of the first sequence, an identification of the second sequence, an identification of the alignment having the smallest error, the alignment error associated with the alignment having the smallest error, a number of gaps in the first sequence, a number of gaps in the second sequence, a position of the alignment having the smallest error, and a beginning position in one of the first sequence and the second sequence of the alignment having the smallest error.

5. (Previously presented) A method according to claim 4, where: mismatches are negative matches, and, the matches can be at least one of perfect matches and positive matches.

6. (Previously presented) A method according to claim 4, where computing a second percent identity relative to the second sequence includes: determining an alignment number based on the matches between the first sequence and the second sequence based on the alignment having the smallest error, and forming a ratio based on the alignment number and a length of the second sequence.

7. (Previously presented) A method according to claim 6, where: mismatches are negative matches, and the matches can be at least one of perfect matches and positive matches.

8. (Currently amended) A method according to claim 6, further including computing by means of at least one processor a third percent identity relative to the alignment having the smallest error.

9. (Previously presented) A method according to claim 8, where computing the third percent identity includes: determining an alignment number based on the matches between the first sequence and the second sequence based on the alignment having the smallest error, and forming a ratio based on the alignment number and a length of the alignment.

10. (Currently amended) A method according to claim 4, further including, determining by means of at least one processor whether at least one of the first percent identity and the second percent identity is greater than a percent identity threshold.

11. (Previously presented) A method according to claim 10, further including providing the percent identity threshold.

12. (Currently amended) A method according to claim 4, further including, for the alignment having the smallest error, determining by means of at least one processor at least one of a number of gaps in the first sequence, a number of gaps in the second sequence, a number based on the gaps in the first sequence, and a number based on the gaps in the second sequence.

13. (Currently amended) A method according to claim 4, further including: providing at least one database in at least one storage means, the at least one database including ~~at least one sequence,~~ a plurality of sequences, and, retrieving to at least one processor at least one of the first sequence and the second sequence from the at least one database.

14. (Previously presented) A method according to claim 4, where, the first sequence comprises at least one sequence chosen from a group comprising: polypeptide sequences and nucleotide sequences, and, the second sequence comprises at least one sequence chosen from a group comprising: polypeptide sequences and nucleotide sequences.

15. (Previously presented) A method according to claim 6, where associating an error with an alignment includes computing an error based on a number of mismatches in the said alignment.

16. (Previously presented) A method according to claim 6, where associating an error with an alignment includes aligning the first sequence with the second sequence based on at least one insertion event in at least one of: the first sequence and the second sequence.

17. (Previously presented) A method according to claim 6, where associating an error with an alignment includes computing a string edit distance.

18. (Previously presented) A method according to claim 6, where associating an error with an alignment includes comparing the said alignment error to an alignment error threshold.

19. (Previously presented) A method according to claim 4, where associating an error with an alignment includes comparing a length of the first sequence to a length of the second sequence to identify a shorter sequence and a longer sequence, and aligning at least the entirety of the shorter sequence with at least a fragment of the longer sequence.

20. (Original) A method according to claim 19, where aligning at least the entirety includes inserting at least one gap into at least one of the shorter sequence and the longer sequence.

21. (Original) A method according to claim 19, where comparing includes, determining that the first sequence length is equal to the second sequence length, and, associating the first sequence with the shorter sequence and the second sequence with the longer sequence, and performing the aligning, and, associating the first sequence with the longer sequence and the second sequence with the shorter sequence, and performing the aligning.

22. (Original) A method according to claim 19, where comparing includes, determining that the first sequence length is equal to the second sequence length, and, associating at least one of: the first sequence with the shorter sequence and the second sequence with the longer sequence, and, the first sequence with the longer sequence and the second sequence with the shorter sequence.

23. – 25. (Canceled)

26. (Currently amended) A method according to claim 4, further including: comparing by means of at least one processor the length of the first sequence with the length of the second sequence, and, performing the alignments based on the length comparison and a percent identity threshold.

27. (Previously presented) A method according to claim 4, further including providing at least one interface to perform at least one of: identify the first sequence, identify the second sequence, provide a percent identity threshold, and provide an alignment error threshold.

28. (Currently amended) A method according to claim 4, further comprising outputting by means of at least one output device the first percent identity and the second percent identity.

29. (Currently amended) A method according to claim 4, further comprising outputting by means of at least one output device the first percent identity and the second percent identity based on at least one of: a percent identity threshold and an alignment error threshold.

30. (Currently amended) A method according to claim 4, further comprising outputting by means of at least one output device a scoring matrix associated with the first percent identity and the second percent identity.

31. (Canceled)

32. (Currently amended) A method according to claim 4, further comprising: iteratively storing in at least one storage means the first percent identity and the second percent identity, retrieving at least one of a new first sequence and a new second sequence, and, repeating steps (a) to (c).

33. (Original) A method according to claim 32, where storing includes associating the first percent identity and the second percent identity with at least one of the first sequence and the second sequence.

34. – 46. (Canceled)

47. (Currently amended) A method for comparing a first sequence and a second sequence, performed on a suitably programmed computer system containing at least one input device, at least one output device, at least one storage means, and at least one processor, the method comprising:

(a) comparing by means of at least one processor a length of the first sequence to a length of the second sequence;

(b) based on the length comparison and a percent identity threshold, determining by means of at least one processor a plurality of alignments of the first sequence with the second sequence,

where determining an alignment comprises, based on the lengths of the first and second sequences, identifying a shorter sequence and a longer sequence and aligning the shorter sequence with at least a fragment of the longer sequence;

(c) for each said alignment of the first sequence with the second sequence, associating an error therewith by means of at least one processor, where associating an error with an alignment includes,

i) computing an error based on a number of mismatches in the said alignment; and

ii) computing an error based on at least one insertion event in at least one of the shorter sequence and the fragment of the longer sequence;

(d) comparing by means of at least one processor the associated alignment errors to identify an alignment having the smallest error, ~~and,~~

(e) based on the alignment having the smallest error, computing by means of at least one processor a first percent identity relative to the first sequence, and a second percent identity relative to the second sequence,

where computing a percent identity relative to a given sequence includes determining an alignment number based on matches between the first sequence and the second sequence based on the alignment having the smallest error, and, forming a ratio based on the alignment number and the length of the given sequence; and

(f) based upon the computed first percent identity and second percent identity outputting a result by means of at least one output device to at least one of a user, a storage device, a computer, or a display,

where outputting a result comprises outputting at least one of a ~~the first~~ percent identity, ~~the second percent identity, a third percent identity,~~ a scoring matrix, an identification of the first sequence, an identification of the second sequence, an identification of the alignment having the smallest error, the alignment error associated with the alignment having the smallest error, a number of gaps in the first sequence, a number of gaps in the second sequence, a position of the alignment having the smallest error, and a beginning position in one of the first sequence and the second sequence of the alignment having the smallest error.

48 (Currently amended) A method according to claim 32, further comprising: sorting by means of at least one processor a plurality of stored first percent identities and second percent identities based on percent identity, and outputting by means of at least

one output device at least one of the sorted first percent identities and second percent identities.

49. (Previously presented) A method according to claim 4, where at least one of the first sequence and the second sequence includes an ASCII string.

50. (Currently amended) A method according to claim 4, further comprising: performing in at least one parallel processing thread by means of at least one processor, iteratively storing the first percent identity and the second percent identity, retrieving at least one of a new first sequence and a new second sequence, and repeating steps (a) to (c).

51. (Previously presented) A method according to claim 49, where at least one of the first sequence and the second sequence is selected from a database of sequences.

52 (Previously presented) A method according to claim 51, where the first sequence is selected from a first database of sequences and the second sequence is selected from a second database of sequences.

53. (Previously presented) A method according to claim 51, where the first sequence and the second sequence are selected from the same database of sequences.

54 (Currently amended) A method according to claim 19, further comprising aligning by means of at least one processor at least the entirety of the shorter sequence with at least the fragment of the longer sequence based on at least one insertion event in at least one of: the entirety of the shorter sequence and at least the fragment of the longer sequence.

55 (Previously presented) A method according to claim 54, where associating an error with an alignment includes computing an error based on a number of mismatches in the alignment.

56. (Previously presented) A method according to claim 54, where associating an error with an alignment includes computing a string edit distance.

57. (Previously presented) A method according to claim 55, where associating an error with an alignment includes comparing the said alignment error to an alignment error threshold.